

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/763,978

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 \_\_\_\_\_ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 \_\_\_\_\_ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 \_\_\_\_\_ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 \_\_\_\_\_ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 \_\_\_\_\_ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 \_\_\_\_\_ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 8 \_\_\_\_\_ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
**(2) INFORMATION FOR SEQ ID NO:X:**  
**(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
**This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 \_\_\_\_\_ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
**<210> sequence id number**  
**<400> sequence id number**  
**000**
- 10 \_\_\_\_\_ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 \_\_\_\_\_ Use of "Artificial" (NEW RULES)      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 \_\_\_\_\_ Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
**Please explain source of genetic material in <220> to <223> section.**  
**(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)**
- 13   ✓   PatentIn ver. 2.0 "bug"      **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/763,978

DATE: 05/16/2001  
TIME: 13:29:15

Input Set : A:\Dex-0043.app

Output Set: N:\CRF3\05162001\I763978.raw

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C--> 2 <141> CURRENT FILING DATE: 2001-02-28  
W--> 2 <151> PRIOR FILING DATE: 1998-09-02  
W--> 0 <110> APPLICANT:  
W--> 0 <120> TITLE INVENTION:  
W--> 0 <130> FILE REFERENCE:  
4 <160> NUMBER OF SEQ ID NOS: 15  
6 <170> SOFTWARE: PatentIn Ver. 2.0  
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Does Not Comply  
Corrected Diskette Needed

see p. 6 for explanation

see  
p. 5, 6

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,978

DATE: 05/16/2001

TIME: 13:29:15

Input Set : A:\Dex-0043.app

Output Set: N:\CRF3\05162001\I763978.raw

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DATE: 05/16/2001

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Input Set : A:\Dex-0043.app

Output Set: N:\CRF3\05162001\I763978.raw

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104 <213> ORGANISM: Homo sapiens
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109 tgtttgtgca ttgggaatga cattctttcc caccacagga aaacctttgg gactttcaga 180
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145 atatcttcta tatttaatat gaaagtcttg aaatgtatca gacagaaggg gatttcagtt 180
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150 <211> LENGTH: 359
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,978

DATE: 05/16/2001

TIME: 13:29:15

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Output Set: N:\CRF3\05162001\I763978.raw

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164 &lt;212&gt; TYPE: DNA

165 &lt;213&gt; ORGANISM: Homo sapiens

167 &lt;220&gt; FEATURE:

168 &lt;221&gt; NAME/KEY: unsure

169 &lt;222&gt; LOCATION: (6)

171 &lt;220&gt; FEATURE:

172 &lt;221&gt; NAME/KEY: unsure

173 &lt;222&gt; LOCATION: (9)

175 &lt;400&gt; SEQUENCE: 6

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181 ttccagaagc atgcggctgc tcctattgct gagctgcctg gccaaaacag gagtcctggg 360
182 tgatatcatc atgagaccca gctgtgctcc tgggatgggt ttaccacaag tccaattgct 420
183 atggttactt caggaagctg aggaactggt ctgatgccga gctcgagtgt cagtcttacg 480
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196 aactcctgct tgtttttctt ttggccatgg gaaggtttac cagtagaatc cttgctaggt 1260
197 tgatgtgggc catacattcc tttataaacc cattgtgtac ataagaggtt gctgtgttcc 1320
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202 &lt;212&gt; TYPE: DNA

203 &lt;213&gt; ORGANISM: Homo sapiens

205 &lt;220&gt; FEATURE:

206 &lt;221&gt; NAME/KEY: unsure

207 &lt;222&gt; LOCATION: (277)

209 &lt;400&gt; SEQUENCE: 7

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DATE: 05/16/2001

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Input Set : A:\Dex-0043.app

Output Set: N:\CRF3\05162001\I763978.raw

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 212 gtcttaggtt tcatcttcag atgactgggt gaacagcagt gttctttgct aagatgggga 180  
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 241 acaaaaactaa aattgttaat tacaagaaaa tatagggtgt taccttttga aggtttatta 480  
 242 atacatatgg ttgtcacaaat acgtatatat gataaatggg gtacatatat agatgtttat 540  
 243 ggtgtataaa tttttctata cccaattaga attatcttcc tgattcttta ttcaataaca 600  
 244 tgctaattcc tcttctatgt tctatagtga cagaatgcta actttttctta taccctggca 660  
 245 gaggacagag gagtctggtc taggatgggg aactgaattt ttgaacgaaa aggaaagaga 720  
 W 246 aaggatggnn nnnnnnnnnn nnnnnnnnnn nnnnnntaat gtttcttagt cattttgatt 780  
 247 ggccatttga acagtctaca agtttaacgt tatttccagt gaagtaggat ggctgacctt 840  
 248 gcaatacatg tttcttcaaa agggtaaaaca tgcttttagt acctaaagct aaatttttga 900  
 W 249 catttgacat caggggtggt ataagtactg cacttaatac aaagctattt ctcaatngtg 960  
 250 ttattttttga gacaaatttt tcttcacat taacttcttg ttggtagctt tttgttttgt 1020  
 251 aaaaattgag agatggcaat gcttatctca accagattat ccatctgcag aattaaggta 1080  
 252 tgcaactggg aaataaaaaga caaatgctcc agtttgtctt tctcaacctt tgagttctta 1140  
 253 acctttgagt taaaacctag tctaaatagt gggaatgtct tggtttacag taagggtttc 1200  
 254 ttgggaagga tcttggtttt gtgatctatt tgtgaattaa ggagtagatg ttaaccatta 1260  
 255 ttttatagat aagtg 1275  
 257 <210> SEQ ID NO: 9  
 258 <211> LENGTH: 2479  
 259 <212> TYPE: DNA  
 260 <213> ORGANISM: Homo sapiens  
 262 <400> SEQUENCE: 9  
 263 gtcattatga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60  
 264 ctttgaactc aggggtacca ccagctattg gaccttacta tgaaaacctt ggataccaac 120  
 265 cggaaaaccc ctatcccgcg cagcccactg tggccccac tgtctacgag gtgcatccgg 180

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the  
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to  
 <223> fields of each sequence which presents at least one n or Xaa.

<1107  
<1207  
<1407  
<1417  
<1507

Insert these  
marks  
numeric identifiers  
and responses' delete this  
~~SEQUENCE LISTING~~

09/763,978 6

☐

<151> 1998-09-02

☐

☐

<160> 15

☐

☐

<170> PatentIn Ver. 2.0

see item 13 on  
Error Summary  
sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/763,978

DATE: 05/16/2001

TIME: 13:29:16

Input Set : A:\Dex-0043.app

Output Set: N:\CRF3\05162001\I763978.raw

L:2 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:2 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:2 M:289 W: Identifier Missing or Out-Of-Order, <150> PRIOR APP NO  
 L:0 M:201 W: Mandatory field data missing, APPLICANT NAME  
 L:0 M:201 W: Mandatory field data missing, TITLE INVENTION  
 L:0 M:201 W: Mandatory field data missing, FILE REFERENCE  
 L:176 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
 L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
 L:214 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
 L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
 L:240 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
 L:240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
 L:246 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
 L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
 L:249 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
 L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
 L:363 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
 L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
 L:367 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
 L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
 L:369 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
 L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12